

C1

(2) INFORMATION FOR SEQ ID NO:1:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 566 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
 (A) NAME/KEY: Peptide
 (B) LOCATION: 1..566
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Ser | Ser | Lys | Lys | Met | Asp | Ala | Ala | Gly | Thr | Leu | Gln | Pro | Asn |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Pro | Leu | Lys | Leu | Gln | Pro | Asp | Arg | Gly | Ala | Gly | Ser | Val | Leu | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Glu | Gln | Gly | Gly | Tyr | Lys | Glu | Lys | Phe | Val | Lys | Thr | Val | Glu | Asp |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Tyr | Lys | Cys | Glu | Lys | Cys | Arg | Leu | Val | Leu | Cys | Asn | Pro | Lys | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Glu | Cys | Gly | His | Arg | Phe | Cys | Glu | Ser | Cys | Met | Ala | Ala | Leu | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Ser | Ser | Ser | Pro | Lys | Cys | Thr | Ala | Cys | Gln | Glu | Ser | Ile | Ile | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Lys | Val | Phe | Lys | Asp | Asn | Cys | Cys | Lys | Arg | Glu | Ile | Leu | Ala | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gln | Val | Tyr | Cys | Arg | Asn | Glu | Gly | Arg | Gly | Cys | Ala | Glu | Gln | Leu | Thr |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Gly | His | Leu | Leu | Val | His | Leu | Lys | Asn | Glu | Cys | Gln | Phe | Glu | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Pro | Cys | Leu | Arg | Ala | Asp | Cys | Lys | Glu | Lys | Val | Leu | Arg | Lys | Asp |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Arg | Asp | His | Val | Glu | Lys | Ala | Cys | Lys | Tyr | Arg | Glu | Ala | Thr | Cys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ser | His | Cys | Lys | Ser | Gln | Val | Pro | Met | Ile | Lys | Leu | Gln | Lys | His | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asp | Thr | Asp | Cys | Pro | Cys | Val | Val | Val | Ser | Cys | Pro | His | Lys | Cys | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Val | Gln | Thr | Leu | Leu | Arg | Ser | Glu | Leu | Ser | Ala | His | Leu | Ser | Glu | Cys |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Asn | Ala | Pro | Ser | Thr | Cys | Ser | Phe | Lys | Arg | Tyr | Gly | Cys | Val | Phe |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Gln | Gly | Thr | Asn | Gln | Gln | Ile | Lys | Ala | His | Glu | Ala | Ser | Ser | Ala | Val |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gln | His | Val | Asn | Leu | Leu | Lys | Glu | Trp | Ser | Asn | Ser | Leu | Glu | Lys | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Ser | Leu | Leu | Gln | Asn | Glu | Ser | Val | Glu | Lys | Asn | Lys | Ser | Ile | Gln |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ser | Leu | His | Asn | Gln | Ile | Cys | Ser | Phe | Glu | Ile | Glu | Ile | Glu | Arg | Gln |

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| 290             | 295                                             | 300                         |
|-----------------|-------------------------------------------------|-----------------------------|
| Lys Glu Met Leu | Arg Asn Asn Glu Ser Lys                         | Ile Leu His Leu Gln Arg     |
| 305             | 310                                             | 315 320                     |
| Val Ile Asp Ser | Gln Ala Glu Lys Leu                             | Lys Glu Leu Asp Lys Glu Ile |
|                 | 325                                             | 330 335                     |
| Arg Pro Phe Arg | Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser Ser |                             |
|                 | 340                                             | 345 350                     |
| Val Glu Ser Leu | Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp Lys |                             |
|                 | 355                                             | 360 365                     |
| Ser Ala Gly Gln | Ala Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu |                             |
|                 | 370                                             | 375 380                     |
| Ser Arg His Asp | Gln Thr Leu Ser Val His Asp Ile Arg Leu Ala Asp |                             |
|                 | 385                                             | 390 395 400                 |
| Met Asp Leu Arg | Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly Val |                             |
|                 | 405                                             | 410 415                     |
| Leu Ile Trp Lys | Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala Val |                             |
|                 | 420                                             | 425 430                     |
| Met Gly Lys Thr | Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr |                             |
|                 | 435                                             | 440 445                     |
| Phe Gly Tyr Lys | Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met |                             |
|                 | 450                                             | 455 460                     |
| Gly Lys Gly Thr | His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu |                             |
|                 | 465                                             | 470 475 480                 |
| Tyr Asp Ala Leu | Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met |                             |
|                 | 485                                             | 490 495                     |
| Leu Met Asp Gln | Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys |                             |
|                 | 500                                             | 505 510                     |
| Pro Asp Pro Asn | Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn |                             |
|                 | 515                                             | 520 525                     |
| Ile Ala Ser Gly | Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn |                             |
|                 | 530                                             | 535 540                     |
| Gly Thr Tyr Ile | Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp |                             |
|                 | 545                                             | 550 555 560                 |
| Thr Ser Asp Leu | Pro Asp                                         |                             |
|                 | 565                                             |                             |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Glu        | Ser        | Ser        | Lys<br>5   | Lys        | Met        | Asp        | Ser        | Pro<br>10  | Gly        | Ala        | Leu        | Gln        | Thr        | Asn<br>15  |
| Pro        | Pro        | Leu        | Lys<br>20  | Leu        | His        | Thr        | Asp        | Arg<br>25  | Ser        | Ala        | Gly        | Thr        | Pro<br>30  | Val        | Phe        |
| Val        | Pro        | Glu<br>35  | Gln        | Gly        | Gly        | Tyr        | Lys<br>40  | Glu        | Lys        | Phe        | Val        | Lys<br>45  | Thr        | Val        | Glu        |
| Asp        | Lys<br>50  | Tyr        | Lys        | Cys        | Glu        | Lys<br>55  | Cys        | His        | Leu        | Val        | Leu<br>60  | Cys        | Ser        | Pro        | Lys        |
| Gln<br>65  | Thr        | Glu        | Cys        | Gly        | His<br>70  | Arg        | Phe        | Cys        | Glu        | Ser<br>75  | Cys        | Met        | Ala        | Ala        | Leu<br>80  |
| Leu        | Ser        | Ser        | Ser        | Ser<br>85  | Pro        | Lys        | Cys        | Thr        | Ala<br>90  | Cys        | Gln        | Glu        | Ser        | Ile<br>95  | Val        |
| Lys        | Asp        | Lys        | Val<br>100 | Phe        | Lys        | Asp        | Asn<br>105 | Cys        | Cys        | Lys        | Arg        | Glu<br>110 | Ile        | Leu        | Ala        |
| Leu        | Gln        | Ile<br>115 | Tyr        | Cys        | Arg        | Asn<br>120 | Glu        | Ser        | Arg        | Gly        | Cys        | Ala<br>125 | Glu        | Gln        | Leu        |
| Thr        | Leu<br>130 | Gly        | His        | Leu        | Leu        | Val<br>135 | His        | Leu        | Lys        | Asn<br>140 | Asp        | Cys        | His        | Phe        | Glu        |
| Glu<br>145 | Leu        | Pro        | Cys        | Val        | Arg<br>150 | Pro        | Asp        | Cys        | Lys        | Glu<br>155 | Lys        | Val        | Leu        | Arg        | Lys<br>160 |
| Asp        | Leu        | Arg        | Asp        | His<br>165 | Val        | Glu        | Lys        | Ala        | Cys<br>170 | Lys        | Tyr        | Arg        | Glu        | Ala<br>175 | Thr        |
| Cys        | Ser        | His        | Cys<br>180 | Lys        | Ser        | Gln        | Val        | Pro<br>185 | Met        | Ile        | Ala        | Leu        | Gln<br>190 | Lys        | His        |
| Glu        | Asp        | Thr<br>195 | Asp        | Cys        | Pro        | Cys        | Val<br>200 | Val        | Val        | Ser        | Cys        | Pro<br>205 | His        | Lys        | Cys        |
| Ser        | Val<br>210 | Gln        | Thr        | Leu        | Leu        | Arg<br>215 | Ser        | Glu        | Leu        | Ser        | Ala<br>220 | His        | Leu        | Ser        | Glu        |
| Cys<br>225 | Val        | Asn        | Ala        | Pro        | Ser<br>230 | Thr        | Cys        | Ser        | Phe        | Lys<br>235 | Arg        | Tyr        | Gly        | Cys        | Val<br>240 |

|                     |                                             |
|---------------------|---------------------------------------------|
| Phe Gln Gly Thr Asn | Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala |
| 245                 | 250 255                                     |
| Val Gln His Val Asn | Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys |
| 260                 | 265 270                                     |
| Lys Val Ser Leu Leu | Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile |
| 275                 | 280 285                                     |
| Gln Ser Leu His Asn | Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg |
| 290                 | 295 300                                     |
| Gln Lys Glu Met Leu | Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln |
| 305                 | 310 315 320                                 |
| Arg Val Ile Asp Ser | Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu |
| 325                 | 330 335                                     |
| Ile Arg Pro Phe Arg | Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser |
| 340                 | 345 350                                     |
| Ser Val Glu Ser Leu | Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp |
| 355                 | 360 365                                     |
| Lys Ser Ala Gly Gln | Val Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln |
| 370                 | 375 380                                     |
| Leu Ser Arg His Asp | Gln Met Leu Ser Val His Asp Ile Arg Leu Ala |
| 385                 | 390 395 400                                 |
| Asp Met Asp Leu Arg | Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly |
| 405                 | 410 415                                     |
| Val Leu Ile Trp Lys | Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala |
| 420                 | 425 430                                     |
| Val Met Gly Lys Thr | Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly |
| 435                 | 440 445                                     |
| Tyr Phe Gly Tyr Lys | Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly |
| 450                 | 455 460                                     |
| Met Gly Lys Gly Thr | His Leu Ser Leu Phe Phe Val Ile Met Arg Gly |
| 465                 | 470 475 480                                 |
| Glu Tyr Asp Ala Leu | Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu |
| 485                 | 490 495                                     |
| Met Leu Met Asp Gln | Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe |
| 500                 | 505 510                                     |
| Lys Pro Asp Pro Asn | Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met |
| 515                 | 520 525                                     |
| Asn Ile Ala Ser Gly | Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu |
| 530                 | 535 540                                     |
| Asn Gly Thr Tyr Ile | Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val |

65711

545

550

555

560

Asp Thr Ser Asp Leu Pro Asp Pro  
565

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| GGCGGCGGAG GATGCGCGCG GCGCCTGAGC CGGCCGAACG GGCGGCCTCG GGGTACAGGG | 60   |
| TCCCCATTAC TTGAAGGATA AGGCTGGCAC GGCTCCGACG TCTGTGTGGA AGCTTCTCCC | 120  |
| TCCCTTCTGA GCTTCTCTAG ACTCCTTACA GCGCACGGCA CAGAATTTCA GTTTCCTAAG | 180  |
| ATGGAGTCAA GCAAAAAGAT GGATGCTGCT GGCACACTGC AGCCTAACCC ACCCCTAAAG | 240  |
| CTGCAGCCTG ATCGCGGCGC AGGGTCCGTG CTCGTGCCGG AGCAAGGAGG CTACAAGGAG | 300  |
| AAGTTTGTGA AGACGGTGGA AGACAAGTAC AAGTGCGAGA AGTGCCGCCT GGTGCTGTGC | 360  |
| AACCCGAAGC AGACGGAGTG TGGCCACCGG TTCTGCGAGA GCTGCATGGC CGCCCTGCTG | 420  |
| AGCTCCTCCA GTCCAAAATG CACAGCGTGC CAAGAAAGCA TCATCAAAGA CAAGGTGTTT | 480  |
| AAGGATAATT GCTGCAAGAG AGAGATTCTG GCCCTTCAGG TCTACTGTCG GAATGAAGGC | 540  |
| AGAGGTTGTG CGGAGCAGCT GACTCTGGGA CATCTGCTGG TGCACCTAAA AAATGAATGT | 600  |
| CAGTTTGAGG AACTTCCCTG TCTGCGTGCC GACTGCAAAG AAAAAGTACT GAGAAAAGAC | 660  |
| TTGCGGGATC ACGTGAAAA GGCCTGTAAA TACCGCGAGG CCACGTGCAG TCACTGCAAG  | 720  |
| AGCCAAGTGC CCATGATCAA ACTGCAGAAA CATGAAGACA CAGATTGTCC CTGTGTGGTG | 780  |
| GTATCCTGCC CTCACAAGTG CAGCGTTCAG ACTCTTCTAA GGAGTGAGTT GAGTGCACAC | 840  |
| TTGTCCGAGT GTGTCAATGC CCCCAGCACC TGTAGTTTAA AGCGCTATGG CTGCGTTTTT | 900  |
| CAGGGTACAA ACCAGCAGAT CAAGGCCCAT GAGGCCAGCT CCGCGGTACA GCACGTGAAC | 960  |
| CTGCTGAAGG AGTGGAGCAA CTCCCTGGAG AAGAAGGTTT CCCTGCTGCA GAATGAAAGT | 1020 |
| GTTGAGAAAA ACAAGAGCAT CCAAAGCCTG CACAACCAGA TCTGCAGCTT TGAGATCGAG | 1080 |
| ATTGAGAGGC AGAAGGAGAT GCTCCGAAAC AACGAGTCCA AGATCCTTCA CCTGCAGCGG | 1140 |

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(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: cDNA

CGGGGGAGCG CGGCGCGGCC GCGCGTGCG CGAGCCGGGG TTGCAGCCCA GCCGGGACTT 60

|            |            |             |            |            |            |      |
|------------|------------|-------------|------------|------------|------------|------|
| TCCAGCCGGC | GGCAGCCGGC | GCGGTCGTCTG | GCTCTTCCCC | GCCCCCGTC  | ATGGGGCAGC | 120  |
| CCGGGGAGCA | GAACGCTGCG | GACCGCGGCG  | GAGGACGCGC | CCGGCGCCCC | TGAGCCGGCC | 180  |
| GAGCGGCGAC | GGACCGCGAG | AACTCCTCTT  | TCCTAAAATG | GAGTCGAGTA | AAAAGATGGA | 240  |
| CTCTCCTGGC | GCGCTGCAGA | CTAACCCGCC  | GCTAAAGCTG | CACACTGACC | GTAGTGCTGG | 300  |
| GACGCCAGTT | TTTGTCCCTG | AACAAGGAGG  | TTACAAGGAA | AAGTTTGTGA | AGACCGTGGA | 360  |
| GGACAAGTAC | AAGTGTGAGA | AGTGCCACCT  | GGTGCTGTGC | AGCCCGAAGC | AGACCGAGTG | 420  |
| TGGGCACCGC | TTCTGCGAGA | GCTGCATGGC  | GGCCCTGCTG | AGCTCTTCAA | GTCCAAAATG | 480  |
| TACAGCGTGT | CAAGAGAGCA | TCGTTAAAGA  | TAAGGTGTTT | AAGGATAATT | GCTGCAAGAG | 540  |
| AGAAATTCTG | GCTCTTCAGA | TCTATTGTCG  | GAATGAAAGC | AGAGGTTGTG | CAGAGCAGTT | 600  |
| AACGCTGGGA | CATCTGCTGG | TGCATTTAAA  | AAATGATTGC | CATTTTGAAG | AACTTCCATG | 660  |
| TGTGCGTCTT | GACTGCAAAG | AAAAGGTCTT  | GAGGAAAGAC | CTGCGAGACC | ACGTGGAGAA | 720  |
| GGCGTGTAAG | TACCGGGAAG | CCACATGCAG  | CCACTGCAAG | AGTCAGGTTT | CGATGATCGC | 780  |
| GCTGCAGAAA | CACGAAGACA | CCGACTGTCC  | CTGCGTGGTG | GTGTCTTGCC | CTCACAAGTG | 840  |
| CAGCGTCCAG | ACTCTCCTGA | GGAGCGAGTT  | GAGTGCACAC | TTGTCAGAGT | GTGTCAATGC | 900  |
| CCCCAGCACC | TGTAGTTTTA | AGCGCTATGG  | CTGCGTTTTT | CAGGGGACAA | ACCAGCAGAT | 960  |
| CAAGGCCAC  | GAGGCCAGCT | CCGCCGTGCA  | GCACGTCAAC | CTGCTGAAGG | AGTGGAGCAA | 1020 |
| CTCGCTCGAA | AAGAAGGTTT | CCTTGTTGCA  | GAATGAAAGT | GTAAGAAAAA | ACAAGAGCAT | 1080 |
| ACAAAGTTTG | CACAATCAGA | TATGTAGCTT  | TGAAATTGAA | ATTGAGAGAC | AAAAGGAAAT | 1140 |
| GCTTCGAAAT | AATGAATCCA | AAATCCTTCA  | TTACAGCGA  | GTGATCGACA | GCCAAGCAGA | 1200 |
| GAAACTGAAG | GAGCTTGACA | AGGAGATCCG  | GCCCTTCCGG | CAGAACTGGG | AGGAAGCAGA | 1260 |
| CAGCATGAAG | AGCAGCGTGG | AGTCCCTCCA  | GAACCGCGTG | ACCGAGCTGG | AGAGCGTGGA | 1320 |
| CAAGAGTGCG | GGGCAAGTGG | CTCGGAACAC  | AGGCCTGCTG | GAGTCCAGC  | TGAGCCGGCA | 1380 |
| TGACCAGATG | CTGAGTGTGC | ACGACATCCG  | CCTAGCCGAC | ATGGACCTGC | GCTTCCAGGT | 1440 |
| CCTGGAGACC | GCCAGCTACA | ATGGAGTGCT  | CATCTGGAAG | ATTCGCGACT | ACAAGCGGCG | 1500 |
| GAAGCAGGAG | GCCGTCATGG | GGAAGACCTT  | GTCCCTTTAC | AGCCAGCCTT | TCTACACTGG | 1560 |
| TTACTTTGGT | TATAAGATGT | GTGCCAGGGT  | CTACCTGAAC | GGGGACGGGA | TGGGGAAGGG | 1620 |
| GACGCACTTG | TCGCTGTTTT | TTGTCATCAT  | GCGTGGAGAA | TATGATGCCC | TGCTTCCTTG | 1680 |
| GCCGTTTAAG | CAGAAAGTGA | CACTCATGCT  | GATGGATCAG | GGGTCCTCTC | GACGTCATTT | 1740 |
| GGGAGATGCA | TTCAAGCCCG | ACCCCAACAG  | CAGCAGCTTC | AAGAAGCCCA | CTGGAGAGAT | 1800 |



GAATATCGCC TCTGGCTGCC CAGTCTTTGT GGCCCAAAC GTTCTAGAAA ATGGGACATA 1860  
TATTAAAGAT GATACAATTT TTATTAAAGT CATAGTGGAT ACTTCGGATC TGCCCGATCC 1920  
CTGATAAGTA GCTGGGGAGG TGGATTTAGC AGAAGGCAAC TCCTCTGGGG GATTTGAACC 1980  
GGTCTGTCTT CACTGAGGTC CTCGCGCTCA GAAAAGGACC TTGTGAGACG GAGGAAGCGG 2040  
CAGAAGGCGG ACGCGTGCCG GCGGGAGGAG CCACGCGTGA GCACACCTGA CACGTTTTAT 2100  
AATAGACTAG CCACACTTCA CTCTGAAGAA TTATTTATCC TTCAACAAGA TAAATATTGC 2160  
TGTCAGAGAA GGTTCATCATT TTCATTTTAA AAGATCTAGT TAATTAAGGT GGAAAACATA 2220  
TATGCTAAAC AAAAGAAACA TGATTTTCTC TCCTTAAACT TGAACACCAA AAAAACACAC 2280  
ACACACACAC ACGTGGGGAT AGCTGGACAT GTCAGCATGT TAAGTAAAAG GAGAATTTAT 2340  
GAAATAGTAA TGCAATTCTG ATATCTTCTT TCTAAAATTC AAGAGTGCAA TTTTGTTTCA 2400  
AATACAGTAT ATTGTCTATT TTTAAGGCCT CCAAAAAAAAAA AAAAAATTCC GGCCG 2455

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Lys Ala Cys Lys Tyr Arg  
1 5

20030309